OM protein - protein search, using sw model

Run on: April 25, 2000, 20:10:14 ; Search time 85.2 Seconds
(without alignments)
176.812 Million cell updates/sec

Title: US-09-125-005-6
Perfect score: 3384
Sequence: 1 MAQSTATSPDGGTTFEHLWS.....PDCKARKQPIKEEFTEAEIH 636

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3384	100.0	636	1	W36184	Human p53 tumour s
2	3367.5	99.5	635	1	W30661	Human NBS-1 alpha
3	3304.5	97.7	637	1	W36182	Monkey p53 tumour
4	3130	92.5	588	1	W36189	Human p53 tumour s
5	3058	90.4	587	1	W36187	Human p53 tumour s
6	2830.5	83.6	589	1	W36185	Mouse p53 tumour s
7	2624	77.5	499	1	W36190	Human p53 tumour s
8	2574	76.1	499	1	W36183	Monkey p53 tumour
9	2330.5	68.9	506	1	W36188	Human p53 tumour s
10	726.5	21.5	401	1	W28487	Human p53 protein
11	725.5	21.4	401	1	W28488	Human p53 protein
12	724.5	21.4	355	1	W13950	Del356-393 modifie
13	724.5	21.4	363	1	W13954	Modified p53 varia
14	724.5	21.4	393	1	R22238	Sequence of 53 kD
15	724.5	21.4	393	1	R26758	p53. Synthetic onc
16	724.5	21.4	393	1	R79658	Human p53 protein
17	724.5	21.4	393	1	R94623	p53 protein. Recom
18	724.5	21.4	393	1	R91933	Wild type p53 prot
19	724.5	21.4	393	1	W02617	Human p53 tumour s
20	724.5	21.4	393	1	W05344	Human p53. New hum
21	724.5	21.4	393	1	W13948	Human wild-type p5
22	724.5	21.4	393	1	W57242	Human p53 protein
23	724.5	21.4	393	1	W57243	Human p53 protein
24	724.5	21.4	393	1	W48658	Amino acid sequenc
25	724.5	21.4	393	1	W69217	Human wild-type p5
26	724.5	21.4	393	1	W69718	Human p53 used in
27	724.5	21.4	393	1	Y03191	Amino acid sequenc
28	724.5	21.4	438	1	R74272	Tumour suppressor
29	724.5	21.4	533	1	W19763	p53-GM-CSF immunos
30	723.5	21.4	363	1	W13971	Modified p53 varia
31	723.5	21.4	393	1	W13949	T284R modified hum
32	723.5	21.4	393	1	W13953	T284K modified hum
33	723.5	21.4	393	1	W57244	Human p53 protein
34	723.5	21.4	393	1	W57245	Human p53 protein
35	723.5	21.4	393	1	W84270	Human p53 protein.
36	723.5	21.4	438	1	R50088	p53 tumour suppres
37	720.5	21.3	363	1	W13972	Modified p53 varia
38	720.5	21.3	393	1	W05347	Human p53 mutant R
39	720.5	21.3	393	1	W13951	Human tumour-deriv
40	720	21.3	354	1	R51874	Human p53 amino ac
41	719.5	21.3	363	1	W13973	Modified p53 varia
42	719.5	21.3	363	1	W13974	Modified p53 varia
43	719.5	21.3	393	1	W05345	Human p53 mutant N
44	719.5	21.3	393	1	W05346	Human p53 mutant R
45	719.5	21.3	393	1	W13968	Modified p53 varia

ALIGNMENTS

RESULT 1
W36184
ID W36184 standard; Protein; 636 AA.
AC W36184;
DT 27-APR-1998 (first entry)
DE Human p53 tumour suppressor-related protein SR-p70a.
KW SR-p70; human; transcription factor; p53; tumour suppressor gene;
KW homology; differential splicing; diagnosis; cancer; neuroblastoma;
KW gene therapy; apoptosis.
OS Homo sapiens.
PN WO9728186-A1.
PD 07-AUG-1997.
PF 03-FEB-1997; F00214.
PR 02-FEB-1996; FR-001309.
PA (SNFI) SANOFI SA.
PI Caput D, Ferrara P, Kaghad AM;
DR WPI; 97-402550/37.
DR N-PSDB; V01498.
PT New polypeptide(s) encoded by the SR-p70 tumour suppressor gene -
PT and related nucleic acid, useful for diagnosis and treatment of
PT tumours
PS Claim 7; Fig 6; 136pp; French.
CC This is the amino acid sequence of the human protein SR-p70a. SR-p70
CC are transcription factors which may control the activity of p53-regulated
CC genes, and are expressed by tumour suppressor genes related to the p53
CC gene family. The gene sequence was isolated from the human colon
CC adenocarcinoma cell line HT-29, using primers V01506-7. The sequence
CC can be used in the diagnosis and monitoring of cancer, especially
CC neuroblastoma. The nucleic acid sequences and corresponding antisense
CC sequences, are also useful in gene therapy, e.g. to regulate apoptosis.
SQ Sequence 636 AA;

Query Match 100.0%; Score 3384; DB 1; Length 636;
Best Local Similarity 100.0%; Pred. No. 1.1e-287;
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 MAQSTATSPDGGTTFEHLWSSLEPDSTYFDLPQSSRGNNEVVGGTDSSMDVFHLEGMTTS 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MAQSTATSPDGGTTFEHLWSSLEPDSTYFDLPQSSRGNNEVVGGTDSSMDVFHLEGMTTS 60

Qy      61 VMAQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYAQPSSTFDTMSPAPVIPSNTD 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 VMAQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYAQPSSTFDTMSPAPVIPSNTD 120

Qy     121 YPGPHHFEVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPV 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 YPGPHHFEVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPV 180

Qy     181 YKKAEHVTDVVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPY 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 YKKAEHVTDVVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPY 240

Qy     241 EPPQVGTEFTTILYNFMCNSSCVGGMNRRPILIIITLEMRDGQVLGRRSFEGRICACPGR 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 EPPQVGTEFTTILYNFMCNSSCVGGMNRRPILIIITLEMRDGQVLGRRSFEGRICACPGR 300
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Qy    301 DRKADEDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGAGVKKRRHGDEDTYYLQVR 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 DRKADEDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGAGVKKRRHGDEDTYYLQVR 360

Qy    361 GRENFEILMKLKESLELMELVPQPLVDSYRQQQQLLQRPSHLQPPSYGPVLSPMNKVHGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GRENFEILMKLKESLELMELVPQPLVDSYRQQQQLLQRPSHLQPPSYGPVLSPMNKVHGG 420

Qy    421 MNKLPSVNQLVGQPPPHSSAATPNLGPVGPGMLNNHGHAVPANGEMSSSHSAQSMVSGSH 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 MNKLPSVNQLVGQPPPHSSAATPNLGPVGPGMLNNHGHAVPANGEMSSSHSAQSMVSGSH 480

Qy    481 CTPPPPYHADPSLVSFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPEQYRMT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CTPPPPYHADPSLVSFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPEQYRMT 540

Qy    541 IWRGLQDLKQGHDYSTAQQLLRSSNAATISIGGSGELQRQRVMEAVHFRVRHTITIPNRG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 IWRGLQDLKQGHDYSTAQQLLRSSNAATISIGGSGELQRQRVMEAVHFRVRHTITIPNRG 600

Qy    601 GPGGGPDEWADFGFDLPDCKARKQPIKEEFTEAEIH 636
          |||||||||||||||||||||||||||||||||||||
Db    601 GPGGGPDEWADFGFDLPDCKARKQPIKEEFTEAEIH 636
```

RESULT 2
W30661
ID W30661 standard; Protein; 635 AA.
AC W30661;
DT 07-APR-1999 (first entry)
DE Human NBS-1 alpha protein.
KW Human; NBS-1; p73; antibody; p53 responsive element; p53 promoter;
KW p53-dependent tumour; growth inhibition.
OS Homo sapiens.
PN WO9851350-A1.
PD 19-NOV-1998.
PF 12-MAY-1998; U09516.
PR 12-MAY-1997; US-046207.
PA (DAND) DANA FARBER CANCER INST INC.
PI Jost C, Kaelin W;
DR WPI; 99-059690/05.
PT Treating subjects using NBS-1 proteins and antibodies - used to
PT interact with p53-responsive genes and inhibit growth of
PT p53-dependent tumour cells
PS Example; Fig 1A; 65pp; English.
CC A method has been developed for treating a subject having a
CC p53-dependent tumour cell. The method comprises: (a) determining the
CC level of NBS-1 protein (also known as p73) expressed in the tumour
CC cell and in a corresponding non-malignant cell; (b) selecting subjects
CC having NBS-1 protein level comparable or below that in a corresponding
CC normal cell; (c) elevating tumour cell NBS-1 level, where NBS-1
CC interacts with p53-responsive promoters. Also described in the present
CC invention is an antibody that specifically binds to NBS-1, and an
CC antibody raised to the carboxy portion of NBS-1. NBS-1 can activate the
CC transcription of p53-responsive genes and can inhibit cell growth in a
CC p53-like manner. The present sequence represents the human NBS-1 alpha
CC protein from the present invention.
SQ Sequence 635 AA;

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  Query Match             99.5%;  Score 3367.5;  DB 1;  Length 635;
  Best Local Similarity   99.8%;  Pred. No. 3.1e-286;
  Matches  635;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy      1 MAQSTATSPDGGTTFEHLWSSLEPDSTYFDLPQSSRGNNEVVGGTDSSMDVFHLEGMTTS 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAQSTATSPDGGTTFEHLWSSLEPDSTYFDLPQSSRGNNEVVGGTDSSMDVFHLEGMTTS 60

Qy     61 VMAQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYAQPSSTFDTMSPAPVIPSNTD 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VMAQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYAQPSSTFDTMSPAPVIPSNTD 120

Qy    121 YPGPHHFEVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPV 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 YPGPHHFEVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPV 180

Qy    181 YKKAEHVTDVVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPY 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 YKKAEHVTDVVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPY 240

Qy    241 EPPQVGTEFTTILYNFMCNSSCVGGMNRRPILIIITLEMRDGQVLGRRSFEGRICACPGR 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 EPPQVGTEFTTILYNFMCNSSCVGGMNRRPILIIITLEMRDGQVLGRRSFEGRICACPGR 300

Qy    301 DRKADEDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGAGVKKRRHGDEDTYYLQVR 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 DRKADEDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGAGVKKRRHGDEDTYYLQVR 360

Qy    361 GRENFEILMKLKESLELMELVPQPLVDSYRQQQQLLQRPSHLQPPSYGPVLSPMNKVHGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GRENFEILMKLKESLELMELVPQPLVDSYRQQQQLLQRPSHLQPPSYGPVLSPMNKVHGG 420

Qy    421 MNKLPSVNQLVGQPPPHSSAATPNLGPVGPGMLNNHGHAVPANGEMSSSHSAQSMVSGSH 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 MNKLPSVNQLVGQPPPHSSAATPNLGPVGPGMLNNHGHAVPANGEMSSSHSAQSMVSGSH 480

Qy    481 CTPPPPYHADPSLVSFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPEQYRMT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CTPPPPYHADPSLVSFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPEQYRMT 540

Qy    541 IWRGLQDLKQGHDYSTAQQLLRSSNAATISIGGSGELQRQRVMEAVHFRVRHTITIPNRG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 IWRGLQDLKQGHDYSTAQQLLRSSNAATISIGGSGELQRQRVMEAVHFRVRHTITIPNR- 600

Qy    601 GPGGGPDEWADFGFDLPDCKARKQPIKEEFTEAEIH 636
          |||||||||||||||||||||||||||||||||||||
Db    600 GPGGGPDEWADFGFDLPDCKARKQPIKEEFTEAEIH 635
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RESULT 3
W36182
ID W36182 standard; Protein; 637 AA.
AC W36182;
DT 27-APR-1998 (first entry)
DE Monkey p53 tumour suppressor-related protein SR-p70a.
KW SR-p70; monkey; transcription factor; p53; tumour suppressor gene;
KW homology; differential splicing; diagnosis; cancer; neuroblastoma;
KW gene therapy; apoptosis.
OS Cercopithecus aethiops.
PN WO9728186-A1.
PD 07-AUG-1997.
PF 03-FEB-1997; F00214.
PR 02-FEB-1996; FR-001309.
PA (SNFI) SANOFI SA.
PI Caput D, Ferrara P, Kaghad AM;
DR WPI; 97-402550/37.
DR N-PSDB; V01496.
PT New polypeptide(s) encoded by the SR-p70 tumour suppressor gene -
PT and related nucleic acid, useful for diagnosis and treatment of
PT tumours
PS Claim 1; Fig 4; 136pp; French.
CC This is the amino acid sequence of the protein SR-p70a from monkey cells.
CC SR-p70 are transcription factors which may control the activity of
CC p53-regulated genes, and are expressed by tumour suppressor genes related
CC to the p53 gene family. The gene sequence was isolated from a cDNA
CC library by sequencing the inserts and comparing to sequence databases.
CC The protein sequence contains regions of homology to the p53 protein.
CC A second sequence (SR-p70b) was also isolated from the library and was
CC caused by differential splicing of the sequence (see V01497). The
CC sequences can be used in the diagnosis and monitoring of cancer,
CC especially neuroblastoma. The nucleic acid sequences and corresponding
CC antisense sequences, are also useful in gene therapy, e.g. to regulate
CC apoptosis.
SQ Sequence 637 AA;

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  Query Match           97.7%;  Score 3304.5;  DB 1;  Length 637;
  Best Local Similarity  97.5%;  Pred. No. 1e-280;
  Matches  621;  Conservative    4;  Mismatches   11;  Indels    1;  Gaps    1;

Qy       1 MAQSTATSPDGGTTFEHLWSSLEPDSTYFDLPQSSRGNNEVVGGTDSSMDVFHLEGMTTS 60
           ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MAQSTTTSPDGGTTFEHLWSSLEPDSTYFDLPQSSRGNNEVVGGTDSSMDVFHLEGMTTS 60

Qy      61 VMAQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYAQPSSTFDTMSPAPVIPSNTD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 VMAQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYAQPSSTFDTMSPAPVIPSNTD 120

Qy     121 YPGPHHFEVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPV 180
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db     121 YPGPHHFEVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSAPPPPGTAIRAMPV 180

Qy     181 YKKAEHVTDVVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPY 240
           |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 YKKAEHVTDIVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPY 240

Qy     241 EPPQVGTEFTTILYNFMCNSSCVGGMNRRPILIIITLEMRDGQVLGRRSFEGRICACPGR 300
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db     241 EPPQVGTEFTTILYNFMCNSSCVGGMNRRPILIIITLETRDGQVLGRRSFEGRICACPGR 300

Qy     301 DRKADEDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGAGVKKRRHGDEDTYYLQVR 360
           |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db     301 DRKADEDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGPGVKKRRHGDEDTYYLQVR 360

Qy     361 GRENFEILMKLKESLELMELVPQPLVDSYRQQQQLLQRPSHLQPPSYGPVLSPMNKVHGG 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GRENFEILMKLKESLELMELVPQPLVDSYRQQQQLLQRPSHLQPPSYGPVLSPMNKVHGG 420

Qy     421 MNKLPSVNQLVGQPPPHSSAATPNLGPVGPGMLNNHGHAVPANGEMSSSHSAQSMVSGSH 480
           :|||||||||||||||||||||||||||||| |||||||||||| ||:||| ||||||||
Db     421 VNKLPSVNQLVGQPPPHSSAATPNLGPVGSGMLNNHGHAVPANSEMTSSHGTQSMVSGSH 480

Qy     481 CTPPPPYHADPSLVSFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPEQYRMT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 CTPPPPYHADPSLVSFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPEQYRMT 540

Qy     541 IWRGLQDLKQGHDY-STAQQLLRSSNAATISIGGSGELQRQRVMEAVHFRVRHTITIPNR 599
           |||||||||||||| : |||||||||| |||||||||||||||||||||||||||||||
Db     541 IWRGLQDLKQGHDYGAAAQQLLRSSNAAAISIGGSGELQRQRVMEAVHFRVRHTITIPNR 600

Qy     600 GGPGGGPDEWADFGFDLPDCKARKQPIKEEFTEAEIH 636
           |||| |||||||||||||||||||||||||||||||||
Db     601 GGPGAGPDEWADFGFDLPDCKARKQPIKEEFTEAEIH 637


RESULT   4
W36189
ID   W36189 standard; Protein; 588 AA.
AC   W36189;
DT   27-APR-1998  (first entry)
DE   Human p53 tumour suppressor-related protein SR-p70f.
KW   SR-p70; human; transcription factor; p53; tumour suppressor gene;
KW   homology; differential splicing; diagnosis; cancer; neuroblastoma;
KW   gene therapy; apoptosis.
OS   Homo sapiens.
PN   WO9728186-A1.
PD   07-AUG-1997.
PF   03-FEB-1997; F00214.
PR   02-FEB-1996; FR-001309.
PA   (SNFI ) SANOFI SA.
PI   Caput D, Ferrara P, Kaghad AM;
DR   WPI; 97-402550/37.
DR   N-PSDB; V01504.
PT   New polypeptide(s) encoded by the SR-p70 tumour suppressor gene -
PT   and related nucleic acid, useful for diagnosis and treatment of
PT   tumours
PS   Claim 1; Page 69-70; 136pp; French.
CC   This is the amino acid sequence of the human protein SR-p70f.  SR-p70 are
CC   transcription factors which may control the activity of p53-regulated
CC   genes, and are expressed by tumour suppressor genes related to the p53
CC   gene family.  The gene sequence was isolated from the human neuroblastoma
CC   cell line SK-N-SH, using primers V01515 and V01518.  The SR-p70f gene
CC   sequence contains a 98 bp deletion between bases 24-25 as compared to
CC   the SR-p70a sequence (V01498).  This deletion causes a loss of the
CC   translation initiation codon found in SR-p70a, resulting in the use of
CC   a downstream ATG (corresponding to an internal Met codon in SR-p70a).
CC   The protein is truncated by 48 amino acids at the N-terminus as compared
CC   to the SR-p70a protein (W36184).  The sequence can be used in the
CC   diagnosis and monitoring of cancer, especially neuroblastoma.  The
CC   nucleic acid sequences and corresponding antisense sequences, are also
CC   useful in gene therapy, e.g. to regulate apoptosis.
SQ   Sequence   588 AA;


  Query Match           92.5%;  Score 3130;  DB 1;  Length 588;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-265;
  Matches  588;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      49 MDVFHLEGMTTSVMAQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYAQPSSTFDT 108
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MDVFHLEGMTTSVMAQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYAQPSSTFDT 60

Qy     109 MSPAPVIPSNTDYPGPHHFEVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSTP 168
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 MSPAPVIPSNTDYPGPHHFEVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSTP 120

Qy     169 PPPGTAIRAMPVYKKAEHVTDVVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLSQYVDD 228
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 PPPGTAIRAMPVYKKAEHVTDVVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLSQYVDD 180

Qy     229 PVTGRQSVVVPYEPPQVGTEFTTILYNFMCNSSCVGGMNRRPILIIITLEMRDGQVLGRR 288
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 PVTGRQSVVVPYEPPQVGTEFTTILYNFMCNSSCVGGMNRRPILIIITLEMRDGQVLGRR 240

Qy     289 SFEGRICACPGRDRKADEDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGAGVKKRR 348
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 SFEGRICACPGRDRKADEDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGAGVKKRR 300

Qy     349 HGDEDTYYLQVRGRENFEILMKLKESLELMELVPQPLVDSYRQQQQLLQRPSHLQPPSYG 408
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 HGDEDTYYLQVRGRENFEILMKLKESLELMELVPQPLVDSYRQQQQLLQRPSHLQPPSYG 360

Qy     409 PVLSPMNKVHGGMNKLPSVNQLVGQPPPHSSAATPNLGPVGPGMLNNHGHAVPANGEMSS 468
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 PVLSPMNKVHGGMNKLPSVNQLVGQPPPHSSAATPNLGPVGPGMLNNHGHAVPANGEMSS 420

Qy     469 SHSAQSMVSGSHCTPPPPYHADPSLVSFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDL 528
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 SHSAQSMVSGSHCTPPPPYHADPSLVSFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDL 480

Qy     529 GALKIPEQYRMTIWRGLQDLKQGHDYSTAQQLLRSSNAATISIGGSGELQRQRVMEAVHF 588
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GALKIPEQYRMTIWRGLQDLKQGHDYSTAQQLLRSSNAATISIGGSGELQRQRVMEAVHF 540

Qy     589 RVRHTITIPNRGGPGGGPDEWADFGFDLPDCKARKQPIKEEFTEAEIH 636
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 RVRHTITIPNRGGPGGGPDEWADFGFDLPDCKARKQPIKEEFTEAEIH 588


RESULT   5
W36187
ID   W36187 standard; Protein; 587 AA.
AC   W36187;
DT   27-APR-1998  (first entry)
DE   Human p53 tumour suppressor-related protein SR-p70d.
KW   SR-p70; human; transcription factor; p53; tumour suppressor gene;
KW   homology; differential splicing; diagnosis; cancer; neuroblastoma;
KW   gene therapy; apoptosis.
OS   Homo sapiens.
PN   WO9728186-A1.
PD   07-AUG-1997.
PF   03-FEB-1997; F00214.
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'R   02-FEB-1996; FR-001309.
'A   (SNFI ) SANOFI SA.
'I   Caput D, Ferrara P, Kaghad AM;
'R   WPI; 97-402550/37.
'R   N-PSDB; V01502.
'T   New polypeptide(s) encoded by the SR-p70 tumour suppressor gene -
'T   and related nucleic acid, useful for diagnosis and treatment of
'T   tumours
'S   Claim 1; Page 62-64; 136pp; French.
'C   This is the amino acid sequence of the human protein SR-p70d.  R-p70 are
'C   transcription factors which may control the activity of p53-regulated
'C   genes, and are expressed by tumour suppressor genes related to the p53
'C   gene family.  The gene sequence was isolated from the human colon
'C   neuroblastoma cell line IMR-32, using primers V01512-13.  The SR-p70d
'C   p[rotein sequence is 49 amino acids shorter with a divergence of the
'C   first 13 amino acids as compared to the SR-p70a protein (W36184).
'C   The sequence can be used in the diagnosis and monitoring of cancer,
'C   especially neuroblastoma.  The nucleic acid sequences and corresponding
'C   antisense sequences, are also useful in gene therapy, e.g. to regulate
'C   apoptosis.
'Q   Sequence   587 AA;


 Query Match            90.4%;  Score 3058;  DB 1;  Length 587;
 Best Local Similarity  100.0%;  Pred. No. 3.3e-259;
 Matches  574;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

'y      63 AQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYAQPSSTFDTMSPAPVIPSNTDYP 122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
'b      14 AQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYAQPSSTFDTMSPAPVIPSNTDYP 73

'y     123 GPHHFEVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYK 182
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
'b      74 GPHHFEVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYK 133

'y     183 KAEHVTDVVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPYEP 242
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
'b     134 KAEHVTDVVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPYEP 193

'y     243 PQVGTEFTTILYNFMCNSSCVGGMNRRPILIIITLEMRDGQVLGRRSFEGRICACPGRDR 302
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
'b     194 PQVGTEFTTILYNFMCNSSCVGGMNRRPILIIITLEMRDGQVLGRRSFEGRICACPGRDR 253

'y     303 KADEDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGAGVKKKRHGDEDTYYLQVRGR 362
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
'b     254 KADEDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGAGVKKRRHGDEDTYYLQVRGR 313

'y     363 ENFEILMKLKESLELMELVPQPLVDSYRQQQQLLQRPSHLQPPSYGPVLSPMNKVHGGMN 422
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
'b     314 ENFEILMKLKESLELMELVPQPLVDSYRQQQQLLQRPSHLQPPSYGPVLSPMNKVHGGMN 373

'y     423 KLPSVNQLVGQPPPHSSAATPNLGPVGPGMLNNHGHAVPANGEMSSSHSAQSMVSGSHCT 482
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
'b     374 KLPSVNQLVGQPPPHSSAATPNLGPVGPGMLNNHGHAVPANGEMSSSHSAQSMVSGSHCT 433

'y     483 PPPPYHADPSLVSFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPEQYRMTIW 542
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
'b     434 PPPPYHADPSLVSFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPEQYRMTIW 493

'y     543 RGLQDLKQGHDYSTAQQLLRSSNAATISIGGSGELQRQRVMEAVHFRVRHTITIPNRGGP 602
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
'b     494 RGLQDLKQGHDYSTAQQLLRSSNAATISIGGSGELQRQRVMEAVHFRVRHTITIPNRGGP 553

'y     603 GGGPDEWADFGFDLPDCKARKQPIKEEFTEAEIH 636
           |||||||||||||||||||||||||||||||||
'b     554 GGGPDEWADFGFDLPDCKARKQPIKEEFTEAEIH 587


ESULT   6
36185
D   W36185 standard; Protein; 589 AA.
C   W36185;
T   27-APR-1998  (first entry)

DE   Mouse p53 tumour suppressor-related protein SR-p70c.
KW   SR-p70; mouse; transcription factor; p53; tumour suppressor gene;
KW   homology; differential splicing; diagnosis; cancer; neuroblastoma;
KW   gene therapy; apoptosis.
OS   Mus musculus.
PN   WO9728186-A1.
PD   07-AUG-1997.
PF   03-FEB-1997; F00214.
PR   02-FEB-1996; FR-001309.
PA   (SNFI ) SANOFI SA.
PI   Caput D, Ferrara P, Kaghad AM;
DR   WPI; 97-402550/37.
DR   N-PSDB; V01499.
PT   New polypeptide(s) encoded by the SR-p70 tumour suppressor gene -
PT   and related nucleic acid, useful for diagnosis and treatment of
PT   tumours
PS   Claim 1; Fig 7; 136pp; French.
CC   This is the amino acid sequence of the mouse protein SR-p70c.  SR-p70
CC   are transcription factors which may control the activity of p53-regulated
CC   genes, and are expressed by tumour suppressor genes related to the p53
CC   gene family.  The gene sequence was isolated from the mouse pituitary
CC   tumour cell line AtT-20, using primers V01508-9.  The sequence can be
CC   used in the diagnosis and monitoring of cancer, especially neuroblastoma.
CC   The nucleic acid sequences and corresponding antisense sequences, are
CC   also useful in gene therapy, e.g. to regulate apoptosis.
SQ   Sequence   589 AA;


  Query Match            83.6%;  Score 2830.5;  DB 1;  Length 589;
  Best Local Similarity  91.7%;  Pred. No. 2.7e-239;
  Matches  531;  Conservative   19;  Mismatches   22;  Indels    7;  Gaps    4;

Qy      63 AQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYAQPSSTFDTMSPAPVIPSNTDYP 122
           |||||||| |||| |||| |||||||||||| |||||||||||||||||||||||||||||
Db      13 AQFNLLSSAMDQMGSRAAPASPYTPEHAASAPTHSPYAQPSSTFDTMSPAPVIPSNTDYP 72

Qy     123 GPHHFEVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYK 182
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73 GPHHFEVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYK 132

Qy     183 KAEHVTDVVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPYEP 242
           |||||||:||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db     133 KAEHVTDIVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLAQYVDDPVTGRQSVVVPYEP 192

Qy     243 PQVGTEFTTILYNFMCNSSCVGGMNRRPILIIITLEMRDGQVLGRRSFEGRICACPGRDR 302
           ||||||||||||||||||||||||||||||:||||| |||||||||||||||||||||||
Db     193 PQVGTEFTTILYNFMCNSSCVGGMNRRPILVIITLETRDGQVLGRRSFEGRICACPGRDR 252

Qy     303 KADEDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGAGVKKRRHGDEDTYYLQVRGR 362
           ||||||||||||||||: |||||||||||||||:||||  |||||||||| :|: ||||
Db     253 KADEDHYREQQALNESTTKNGAASKRAFKQSPPAIPALGTNVKKRRHGDEDMFYMHVRGR 312

Qy     363 ENFEILMKLKESLELMELVPQPLVDSYR--QQQQLLQRPSHLQPPSYGPVLSPMNKVHGG 420
           ||||||||:||||||||||||||||||||  |||||||||||||||||||||||||||||
Db     313 ENFEILMKVKESLELMELVPQPLVDSYRQQQQQQQLLQRPSHLQPPSYGPVLSPMNKVHGG 372

Qy     421 MNKLPSVNQLVGQPPPHSSAATPNLGPVGPGMLNNHGHAVPANGEMSSSHSAQSMVSGSH 480
           :|||||||||||||||||| |||||:| ||||:|||::|||||:  ||:|:||||||
Db     373 VNKLPSVNQLVGQPPPHSSAAGPNLGPMGSGMLNSHGHSMPANGEMNGGHSSQTMVSGSH 432

Qy     481 CTPPPPYHADPSLVSFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPEQYRMT 540
           |||||||||||||||||||||||||||| ||||||||||||||||||||:|:|||||
Db     433 CTPPPPYHADPSLVSFLTGLGCPNCIECFTSQGLQSIYHLQNLTIEDLGALKVPDQYRMT 492

Qy     541 IWRGLQDLKQGHDYSTAQQLLR-SSNAATISIGGSGELQRQRVMEAVHFRVRHTITIPNR 599
           |||||||||| ||    ||||| ||||||||||||||||||||||||||||||||||||
Db     493 IWRGLQDLKQSHD--CGQQLLRSSSNAATISIGGSGELQRQRVMEAVHFRVRHTITIPNR 550

Qy     600 GGPGG--GPDEWADFGFDLPDCKARKQPIKEEFTEAEIH 636
           || |   |||||||||||||:|||||||||| | |
Db     551 GGAGAVTGPDEWADFGFDLPDCKSRKQPIKEEFTETESH 589
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RESULT   7
W36190
ID   W36190 standard; Protein; 499 AA.
AC   W36190;
DT   27-APR-1998  (first entry)
DE   Human p53 tumour suppressor-related protein SR-p70b.
KW   SR-p70; human; transcription factor; p53; tumour suppressor gene;
KW   homology; differential splicing; diagnosis; cancer; neuroblastoma;
KW   gene therapy; apoptosis.
OS   Homo sapiens.
PN   WO9728186-A1.
PD   07-AUG-1997.
PF   03-FEB-1997; F00214.
PR   02-FEB-1996; FR-001309.
PA   (SNFI ) SANOFI SA.
PI   Caput D, Ferrara P, Kaghad AM;
DR   WPI; 97-402550/37.
DR   N-PSDB; V01505.
PT   New polypeptide(s) encoded by the SR-p70 tumour suppressor gene -
PT   and related nucleic acid, useful for diagnosis and treatment of
PT   tumours
PS   Claim 1; Page 72-73; 136pp; French.
CC   This is the amino acid sequence of the human protein SR-p70b.  SR-p70 are
CC   transcription factors which may control the activity of p53-regulated
CC   genes, and are expressed by tumour suppressor genes related to the p53
CC   gene family.  The gene sequence was isolated from the human neuroblastoma
CC   cell line SK-N-SH, using primers V01515 and V01518.  The SR-p70b gene
CC   sequence contains a 94 bp deletion between bases 1516-1517 as compared
CC   to the SR-p70a sequence (V01498).  This deletion causes a reading frame
CC   shift resulting in the generation of a stop codon at position 1498-1500.
CC   The resultant protein is truncated by 137 amino acids as compared to the
CC   SR-p70a protein (W36184).  The sequence can be used in the diagnosis and
CC   monitoring of cancer, especially neuroblastoma.  The nucleic acid
CC   sequences and corresponding antisense sequences, are also useful in gene
CC   therapy, e.g. to regulate apoptosis.
SQ   Sequence   499 AA;

  Query Match             77.5%;  Score 2624;  DB 1;  Length 499;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-221;
  Matches  494;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MAQSTATSPDGGTTFEHLWSSLEPDSTYFDLPQSSRGNNEVVGGTDSSMDVFHLEGMTTS 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MAQSTATSPDGGTTFEHLWSSLEPDSTYFDLPQSSRGNNEVVGGTDSSMDVFHLEGMTTS 60

Qy      61 VMAQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYAQPSSTFDTMSPAPVIPSNTD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 VMAQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYAQPSSTFDTMSPAPVIPSNTD 120

Qy     121 YPGPHHFEVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPV 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 YPGPHHFEVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPV 180

Qy     181 YKKAEHVTDVVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPY 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 YKKAEHVTDVVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPY 240

Qy     241 EPPQVGTEFTTILYNFMCNSSCVGGMNRRPILIIITLEMRDGQVLGRRSFEGRICACPGR 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 EPPQVGTEFTTILYNFMCNSSCVGGMNRRPILIIITLEMRDGQVLGRRSFEGRICACPGR 300

Qy     301 DRKADEDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGAGVKKRRHGDEDTYYLQVR 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 DRKADEDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGAGVKKRRHGDEDTYYLQVR 360

Qy     361 GRENFEILMKLKESLELMELVPQPLVDSYRQQQQLLQRPSHLQPPSYGPVLSPMNKVHGG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GRENFEILMKLKESLELMELVPQPLVDSYRQQQQLLQRPSHLQPPSYGPVLSPMNKVHGG 420

Qy     421 MNKLPSVNQLVGQPPPHSSAATPNLGPVGPGMLNNHGHAVPANGEMSSSHSAQSMVSGSH 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 MNKLPSVNQLVGQPPPHSSAATPNLGPVGPGMLNNHGHAVPANGEMSSSHSAQSMVSGSH 480

Qy     481 CTPPPPYHADPSLV 494
           ||||||||||||||
Db     481 CTPPPPYHADPSLV 494


RESULT   8
W36183
ID   W36183 standard; Protein; 499 AA.
AC   W36183;
DT   27-APR-1998  (first entry)
DE   Monkey p53 tumour suppressor-related protein SR-p70b.
KW   SR-p70; monkey; transcription factor; p53; tumour suppressor gene;
KW   homology; differential splicing; diagnosis; cancer; neuroblastoma;
KW   gene therapy; apoptosis.
OS   Cercopithecus aethiops.
PN   WO9728186-A1.
PD   07-AUG-1997.
PF   03-FEB-1997; F00214.
PR   02-FEB-1996; FR-001309.
PA   (SNFI ) SANOFI SA.
PI   Caput D, Ferrara P, Kaghad AM;
DR   WPI; 97-402550/37.
DR   N-PSDB; V01497.
PT   New polypeptide(s) encoded by the SR-p70 tumour suppressor gene -
PT   and related nucleic acid, useful for diagnosis and treatment of
PT   tumours
PS   Claim 1; Fig 5; 136pp; French.
CC   This is the amino acid sequence of the protein SR-p70b from monkey cells.
CC   SR-p70 are transcription factors which may control the activity of
CC   p53-regulated genes, and are expressed by tumour suppressor genes related
CC   to the p53 gene family.  The gene sequence was isolated from a cDNA
CC   library by sequencing the inserts and comparing to sequence databases.
CC   The protein sequence contains regions of homology to the p53 protein.
CC   The SR-p70b gene sequence was isolated simultaneously with the SR-p70a
CC   sequence (V01496) from the library and is created by differential
CC   splicing of the SR-p70 mRNA sequence.  The sequences can be used in the
CC   diagnosis and monitoring of cancer, especially neuroblastoma.  The
CC   nucleic acid sequences and corresponding antisense sequences, are also
CC   useful in gene therapy, e.g. to regulate apoptosis.
SQ   Sequence   499 AA;

  Query Match             76.1%;  Score 2574;  DB 1;  Length 499;
  Best Local Similarity   97.8%;  Pred. No. 5.8e-217;
  Matches  483;  Conservative    3;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       1 MAQSTATSPDGGTTFEHLWSSLEPDSTYFDLPQSSRGNNEVVGGTDSSMDVFHLEGMTTS 60
           |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MAQSTTTSPDGGTTFEHLWSSLEPDSTYFDLPQSSRGNNEVVGGTDSSMDVFHLEGMTTS 60

Qy      61 VMAQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYAQPSSTFDTMSPAPVIPSNTD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 VMAQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYAQPSSTFDTMSPAPVIPSNTD 120

Qy     121 YPGPHHFEVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPV 180
           |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db     121 YPGPHHFEVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSAPPPPGTAIRAMPV 180

Qy     181 YKKAEHVTDVVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPY 240
           |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 YKKAEHVTDIVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPY 240

Qy     241 EPPQVGTEFTTILYNFMCNSSCVGGMNRRPILIIITLETRDGQVLGRRSFEGRICACPGR 300
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db     241 EPPQVGTEFTTILYNFMCNSSCVGGMNRRPILIIITLETRDGQVLGRRSFEGRICACPGR 300

Qy     301 DRKADEDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGAGVKKRRHGDEDTYYLQVR 360
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db     301 DRKADEDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGPGVKKRRHGDEDTYYLQVR 360

Qy     361 GRENFEILMKLKESLELMELVPQPLVDSYRQQQQLLQRPSHLQPPSYGPVLSPMNKVHGG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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D    361 GRENFEILMKLKESLELMELVPQPLVDSYRQQQQLLQRPSHLQPPSYGPVLSPMNKVHGG 420

Y    421 MNKLPSVNQLVGQPPPHSSAATPNLGPVGPGMLNNHGHAVPANGEMSSSHSAQSMVSGSH 480
         :|||||||||||||||||||||||||||| |||||||||||| ||:|||  ||||||||
D    421 VNKLPSVNQLVGQPPPHSSAATPNLGPVGSGMLNNHGHAVPANSEMTSSHGTQSMVSGSH 480

Y    481 CTPPPPYHADPSLV 494
         ||||||||||||||
D    481 CTPPPPYHADPSLV 494


ESULT   9
36188
D   W36188 standard; Protein; 506 AA.
C   W36188;
T   27-APR-1998  (first entry)
E   Human p53 tumour suppressor-related protein SR-p70e.
W   SR-p70; human; transcription factor; p53; tumour suppressor gene;
W   homology; differential splicing; diagnosis; cancer; neuroblastoma;
W   gene therapy; apoptosis.
S   Homo sapiens.
N   WO9728186-A1.
D   07-AUG-1997.
F   03-FEB-1997; F00214.
R   02-FEB-1996; FR-001309.
A   (SNFI ) SANOFI SA.
I   Caput D, Ferrara P, Kaghad AM;
R   WPI; 97-402550/37.
R   N-PSDB; V01503.
T   New polypeptide(s) encoded by the SR-p70 tumour suppressor gene -
T   and related nucleic acid, useful for diagnosis and treatment of
T   tumours
S   Claim 1; Page 65-66; 136pp; French.
    This is the amino acid sequence of the human protein SR-p70e.  SR-p70 are
    transcription factors which may control the activity of p53-regulated
    genes, and are expressed by tumour suppressor genes related to the p53
    gene family.  The gene sequence was isolated from the human neuroblastoma
    cell line IMR-32, using primers V01515 and V01518.  The SR-p70e gene
    sequence is identical to the SR-p70d sequence (V01502) except for 2
    deletions of 149 bp and 94 bp between bases 1049-1050 and 1188-1189
    respectively.  The encoded protein is 49 amino acids shorter with a
    divergence of the first 13 amino acids and a divergence between amino
    acids 350-397 as compared to the SR-p70a protein (W36184).  The sequence
    can be used in the diagnosis and monitoring of cancer, especially
    neuroblastoma.  The nucleic acid sequences and corresponding antisense
    sequences, are also useful in gene therapy, e.g. to regulate apoptosis.
)   Sequence   506 AA;


 Query Match             68.9%;  Score 2330.5;  DB 1;  Length 506;
 Best Local Similarity   80.7%;  Pred. No. 1.2e-195;
 Matches  464;  Conservative    1;  Mismatches   27;  Indels   83;  Gaps    6;

r     63 AQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYAQPSSTFDTMSPAPVIPSNTDYP 122
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)     14 AQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYAQPSSTFDTMSPAPVIPSNTDYP 73

r    123 GPHHFEVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYK 182
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)     74 GPHHFEVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYK 133

r    183 KAEHVTDVVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPYEP 242
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)    134 KAEHVTDVVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPYEP 193

r    243 PQVGTEFTTILYNFMCNSSCVGGMNRRPILIIITLEMRDGQVLGRRSFEGRICACPGRDR 302
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)    194 PQVGTEFTTILYNFMCNSSCVGGMNRRPILIIITLEMRDGQVLGRRSFEGRICACPGRDR 253

r    303 KADEDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGAGVKKRRHGDEDTYYLQVRGR 362
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)    254 KADEDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGAGVKKRRHGDEDTYYLQVRGR 313
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Qy    363 ENFEILMKLKESLELMELVPQPLVDSYRQQQQLLQRPSHLQPPSYGPVLSPMNKVHGGMN 422
         ||||||||||||||||||||||||||||||||||||
Db    314 ENFEILMKLKESLELMELVPQPLVDSYRQQQQLLQRP---------------------- 351

Qy    423 KLPSVNQLVGQPPPHS-SAATPNLGPVGPGMLNNHGHAVPANGEMSSSHSAQSMVSGSHC 481
           |   |   || | | |       | |     ||  ||                    |
Db    351 --PRDAQ---QPWPRSASQRRDEQQPQRP----VHGLGVPL----------------HS 384

Qy    482 TPPPPYHADPSLVSFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPEQYRMTI 541
           | |    |                                :|||||||||||||||
Db    385 ATPLPRRPQPR--------------------------------QDLGALKIPEQYRMTI 411

Qy    542 WRGLQDLKQGHDYSTAQQLLRSSNAATISIGGSGELQRQRVMEAVHFRVRHTITIPNRGG 601
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    412 WRGLQDLKQGHDYSTAQQLLRSSNAATISIGGSGELQRQRVMEAVHFRVRHTITIPNRGG 471

Qy    602 PGGGPDEWADFGFDLPDCKARKQPIKEEFTEAEIH 636
         |||||||||||||||||||||||||||||||||||
Db    472 PGGGPDEWADFGFDLPDCKARKQPIKEEFTEAEIH 506


RESULT  10
W28487
ID   W28487 standard; Protein; 401 AA.
AC   W28487;
DT   25-NOV-1997  (first entry)
DE   Human p53 protein variant V-393 encoded by pEC145.
KW   Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;
KW   substitution; replacement; transactivation; viral protein VP16; HSV;
KW   anti-oncogene; hyperproliferation; cancer; restenosis;
KW   tumour suppression; apoptosis.
OS   Chimeric - Homo sapiens.
OS   Chimeric - Herpes simplex virus.
OS   Synthetic.
PN   WO9704092-A1.
PD   06-FEB-1997.
PF   17-JUL-1996; F01111.
PR   19-JUL-1995; FR-008729.
PA   (RHON ) RHONE POULENC RORER SA.
PI   Bracco L,  Conseiller E;
DR   WPI; 97-132633/12.
DR   N-PSDB; T86219.
PT   New p53 variants e.g. with oligomerisation domain replaced by
PT   leucine zipper - useful for treating hyper-proliferative disorders,
PT   esp. cancer and restenosis
PS   Claim 34; Pages 83-85; 133pp; French.
CC   Claimed variants of protein p53 have at least part of the p53
CC   transactivation domain (amino acids 1-74) deleted and replaced by
CC   the transactivating domain (TD) from herpes simplex virus viral
CC   protein VP16 (amino acids 411-490). The present sequence is that of
CC   a specifically claimed p53 variant designated V-393 and comprising
CC   the VP16 TD with amino acids 75-393 of human wild-type p53. The p53
CC   variants are more active and more stable tumour suppressors and
CC   apoptosis-inducing agents than wild-type p53 and are active where
CC   the wild-type protein is not.
SQ   Sequence   401 AA;


  Query Match             21.5%;  Score 726.5;  DB 1;  Length 401;
  Best Local Similarity   44.1%;  Pred. No. 1.9e-55;
  Matches  162;  Conservative   56;  Mismatches   94;  Indels   55;  Gaps   11;

Qy      29 FDLPQSSRGNNEVVGGT--DSS------MDVFHLEGMTTSVMAQFNLLSSTMDQMSSRAA 80
           |||    |::   | |  ||:       |  |  | | |  :          :|:    | |
Db      33 FDLDMLGDGDSPGPGFTPHDSAPYGALDMADFEFEQMFTDALG--------IDEYGGRPA 84

Qy      81 SASPYTPEHAASVPTHSPYAQPSSTFDTMSPAPVIPSNTDYPGPHHFEVTFQQSSTAKSA 140
           |:| ||    : |  :|    ||:         :||   | | : | : |  | ||||
Db      85 PAAP-TP----AAPAPAPSWPLSSS---------VPSQKTYQGSYGFRLGFLHSGTAKSV 130

Qy     141 TWTYSPLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYKKAEHVTDVVKRCPNHELG 200
           | |||| | |::||:|||||:|: | : ||||| :||| :||:::|:|:||:|||:||
Db     131 TCTYSPALNKMFCQLAKTCPVQLWVDSTPPPGTRVRAMAIYKQSQHMTEVVRRCPHHERC 190
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Qy    201 RDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPYEPPQVGTEFTTILYNFMCNS 260
          | ::|  ||  |||||||||   :|:||  | | ||||||||||:||:: ||| ||:|||| 
Db    191 SD-SDG-LAPPQHLIRVEGNLRVEYLDDRNTFRHSVVVPYEPPEVGSDCTTIHYNYMCNS 248

Qy    261 SCVGGMNRRPILIIITLEMRDGQVLGRRSFEGRICACPGRDRKADEDHYREQQALNESSA 320
          ||:|||||||||| |||||   | :||| ||| |:||||||||: :|:: |
Db    249 SCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVCACPGRDRRTEEENLR---------- 299

Qy    321 KNG--------AASKRAFKQSPPAVPALGAGVKKRRHGDEDTYYLQVRGRENFEILMKLK 372
          | |         ::|||   :  : |       |::  | : : ||:|||| ||:  :|
Db    299 KKGEPHHELPPGSTKRALPNNTSSSPQ-----PKKKPLDGEYFTLQIRGRERFEMFRELN 353

Qy    373 ESLELME 379
          |:||| :
Db    354 EALELKD 360


RESULT 11
W28488
ID   W28488 standard; Protein; 401 AA.
AC   W28488;
DT   25-NOV-1997  (first entry)
DE   Human p53 protein variant V-393H.
KW   Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;
KW   substitution; replacement; transactivation; viral protein VP16; HSV;
KW   anti-oncogene; hyperproliferation; cancer; restenosis;
KW   tumour suppression; apoptosis.
OS   Chimeric - Homo sapiens.
OS   Chimeric - Herpes simplex virus.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   misc_difference 189
FT                   /note= "Arg residue at position 182 of wild-type
FT                   p53 has been mutated to His"
PN   WO9704092-A1.
PD   06-FEB-1997.
PF   17-JUL-1996; F01111.
PR   19-JUL-1995; FR-008729.
PA   (RHON ) RHONE POULENC RORER SA.
PI   Bracco L,  Conseiller E;
DR   WPI; 97-132633/12.
PT   New p53 variants e.g. with oligomerisation domain replaced by
PT   leucine zipper - useful for treating hyper-proliferative disorders,
PT   esp. cancer and restenosis
PS   Claim 34; Page -; 133pp; French.
CC   Claimed variants of protein p53 have at least part of the p53
CC   transactivation domain (amino acids 1-74) deleted and replaced by
CC   the transactivating domain (TD) from herpes simplex virus viral
CC   protein VP16 (amino acids 411-490). The present sequence is that of
CC   a specifically claimed p53 variant designated V-393H and comprising
CC   the VP16 TD with amino acids 75-393 of human wild-type p53 (but with
CC   Arg182 replaced by His). The p53 variants are more active and more
CC   stable tumour suppressors and apoptosis-inducing agents than wild-type
CC   p53 and are active where the wild-type protein is not.
CC   (Note: this sequence does not appear in the specification and has
CC   been produced by modifying the given sequence of variant V-393).
SQ   Sequence   401 AA;


  Query Match             21.4%;  Score 725.5;  DB 1;  Length 401;
  Best Local Similarity   44.1%;  Pred. No. 2.4e-55;
  Matches  162;  Conservative   56;  Mismatches   94;  Indels   55;  Gaps   11;

Qy     29 FDLPQSSRGNNEVVGGT--DSS------MDVFHLEGMTTSVMAQFNLLSSTMDQMSSRAA 80
          |||    |::   | |  ||:      |  | | | | :          :|:   | |
Db     33 FDLDMLGDGDSPGPGFTPHDSAPYGALDMADFEFEQMFTDALG--------IDEYGGRPA 84

Qy     81 SASPYTPEHAASVPTHSPYAQPSSTFDTMSPAPVIPSNTDYPGPHHFEVTFQQSSTAKSA 140
          |:| ||    : |  :|    ||:         :||   | | : | : |  | ||||
Db     85 PAAP-TP----AAPAPAPSWPLSSS---------VPSQKTYQGSYGFRLGFLHSGTAKSV 130

Qy    141 TWTYSPLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYKKAEHVTDVVKRCPNHELG 200
          | |||| | |::||:|||||:|: | : ||||| :||| :||:::|:|:||:|||:||
Db    131 TCTYSPALNKMFCQLAKTCPVQLWVDSTPPPGTRVRAMAIYKQSQHMTEVVRRCPHHEHC 190

Qy    201 RDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPYEPPQVGTEFTTILYNFMCNS 260
          | ::|  ||  |||||||||   :|:||  | | ||||||||||:||:: ||| ||:|||| 
Db    191 SD-SDG-LAPPQHLIRVEGNLRVEYLDDRNTFRHSVVVPYEPPEVGSDCTTIHYNYMCNS 248

Qy    261 SCVGGMNRRPILIIITLEMRDGQVLGRRSFEGRICACPGRDRKADEDHYREQQALNESSA 320
          ||:|||||||||| |||||   | :||| ||| |:||||||||: :|:: |
Db    249 SCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVCACPGRDRRTEEENLR---------- 299

Qy    321 KNG--------AASKRAFKQSPPAVPALGAGVKKRRHGDEDTYYLQVRGRENFEILMKLK 372
          | |         ::|||   :  : |       |::  | : : ||:|||| ||:  :|
Db    299 KKGEPHHELPPGSTKRALPNNTSSSPQ-----PKKKPLDGEYFTLQIRGRERFEMFRELN 353

Qy    373 ESLELME 379
          |:||| :
Db    354 EALELKD 360


RESULT 12
W13950
ID   W13950 standard; Protein; 355 AA.
AC   W13950;
DT   25-JUN-1997  (first entry)
DE   Del356-393 modified human p53.
KW   p53; tumour suppressor; cancer; therapy; cell proliferation;
KW   apoptosis; protein engineering; DNA binding.
OS   Synthetic.
PN   WO9710843-A1.
PD   27-MAR-1997.
PF   20-SEP-1996; U15188.
PR   22-SEP-1995; US-004802.
PR   21-AUG-1996; US-697221.
PA   (WIST-) WISTAR INST ANATOMY & BIOLOGY.
PI   Halazonetis TD;
DR   WPI; 97-202618/18.
PT   R284K modified p53 protein having DNA binding ability - useful in
PT   treatment of cancer
PS   Claim 3; Refer to Page 27-29; 82pp; English.
CC   Del356-393 modified p53 (W13950) has the C-terminal region of
CC   wild-type human p53 tumour suppressor (W13948) deleted.  Modified
CC   p53 constructs (see also W13954, W13956-61, W13971-77) bearing
CC   a deletion of all or a fragment of the C-terminal residues
CC   356-393 have DNA binding ability and can activate the DNA binding
CC   of common Class I p53 tumour mutants (see also W13951-52).  The
CC   method provides the means for pharmacological rescue of p53
CC   function in cancer patients.  Nucleic acids coding for such
CC   constructs can be used for cancer gene therapy.
SQ   Sequence   355 AA;


  Query Match             21.4%;  Score 724.5;  DB 1;  Length 355;
  Best Local Similarity   42.1%;  Pred. No. 2.4e-55;
  Matches  160;  Conservative   58;  Mismatches  103;  Indels   59;  Gaps   10;

Qy     14 TFEHLWSSLEPDSTYFDLPQSSRGNNEVVGGTDSSMDVFHLEGMTTSVMAQFNLLSSTMD 73
          ||  ||  |  ::    ||  |:  ::::   |              : |:       |
Db     18 TFSDLWKLLPENNVLSPLP--SQAMDDLMLSPDD-------------IEQWFTEDPGPD 61

Qy     74 QMSSRAASASPYTPEHAASVPTHSPYAQPSSTFDTMSPAP------VIPSNTDYPGPHHF 127
          :      :| |  |  ||  |     | |       :|||       :||   | | : |
Db     62 EAPRMPEAAPPVAPAPAAPTP-----AAP-------APAPSWPLSSSVPSQKTYQGSYGF 109

Qy    128 EVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYKKAEHV 187
          : |  | |||| | |||| | |::||:|||||:|: | : ||||| :||| :||:::|:
Db    110 RLGFLHSGTAKSVTCTYSPALNKMFCQLAKTCPVQLWVDSTPPPGTRVRAMAIYKQSQHM 169

Qy    188 TDVVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPYEPPQVGT 247
          |:||:|||:||   | ::|  ||  ||||||||   :|:||  | | ||||||||:||:: 
Db    170 TEVVRRCPHHERCSD-SDG-LAPPQHLIRVEGNLRVEYLDDRNTFRHSVVVPYEPPEVGS 227

Qy    248 EFTTILYNFMCNSSCVGGMNRRPILIIITLEMRDGQVLGRRSFEGRICACPGRDRKADED 307
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        : ||| ||:||||||:||||||||| |||||   | :||| ||| |:||||||||: :|:
Db    228 DCTTIHYNYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVCACPGRDRRTEEE 287

Qy    308 HYREQQALNESSAKNG--------AASKRAFKQSPPAVPALGAGVKKRRHGDEDTYYLQV 359
          : |          | |           ::|||   :  : |        |::  | : : ||:
Db    288 NLR----------KKGEPHHELPPGSTKRALPNNTSSSPQ-----PKKKPLDGEYFTLQI 332

Qy    360 RGRENFEILMKLKESLELME 379
          |||| ||:  :| |:||| :
Db    333 RGRERFEMFRELNEALELKD 352


RESULT 13
W13954
ID   W13954 standard; Protein; 363 AA.
AC   W13954;
DT   25-JUN-1997 (first entry)
DE   Modified p53 variant (del364-393).
KW   p53; tumour suppressor; cancer; therapy; cell proliferation;
KW   apoptosis; protein engineering; DNA binding.
OS   Synthetic.
PN   WO9710843-A1.
PD   27-MAR-1997.
PF   20-SEP-1996; U15188.
PR   22-SEP-1995; US-004802.
PR   21-AUG-1996; US-697221.
PA   (WIST-) WISTAR INST ANATOMY & BIOLOGY.
PI   Halazonetis TD;
DR   WPI; 97-202618/18.
PT   R284K modified p53 protein having DNA binding ability - useful in
PT   treatment of cancer
PS   Example 1; 49-51; 82pp; English.
CC   A modified p53 variant (W13954) comprises wild-type p53 (see
CC   also W13948) having a deletion of the C-terminal 30 amino acids,
CC   and is obtd. by site-directed mutagenesis of p53 DNA. Deletion of
CC   the p53 C-terminal 30 amino acids activates the DNA binding of
CC   common Class I p53 mutants (see also W13951-52). Novel modified
CC   p53 variants (W13949-50, W13953-54, W13968-77), some contg.
CC   C-terminal deletions, provide the means for pharmacological rescue
CC   of p53 function in cancer patients. Nucleic acids coding for
CC   modified p53 can be used for cancer gene therapy.
SQ   Sequence  363 AA;

  Query Match             21.4%;  Score 724.5;  DB 1;  Length 363;
  Best Local Similarity   42.1%;  Pred. No. 2.5e-55;
  Matches  160;  Conservative   58;  Mismatches  103;  Indels   59;  Gaps   10;

Qy     14 TFEHLWSSLEPDSTYFDLPQSSRGNNEVVGGTDSSMDVFHLEGMTTSVMAQFNLLSSTMD 73
          ||  ||  |  ::    ||  |:  ::::   |              : |:          |
Db     18 TFSDLWKLLPENNVLSPLP--SQAMDDLMLSPDD-------------IEQWFTEDPGPD 61

Qy     74 QMSSRAASASPYTPEHAASVPTHSPYAQPSSTFDTMSPAP------VIPSNTDYPGPHHF 127
          :      :| |  |  ||  |     | |       :|||       :||   | | : |
Db     62 EAPRMPEAAPPVAPAPAAPTP-----AAP-------APAPSWPLSSSVPSQKTYQGSYGF 109

Qy    128 EVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYKKAEHV 187
          : |  | |||| | |||| | |::||:|||||:|: | : ||||| :||| :||:::|:
Db    110 RLGFLHSGTAKSVTCTYSPALNKMFCQLAKTCPVQLWVDSTPPPGTRVRAMAIYKQSQHM 169

Qy    188 TDVVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPYEPPQVGT 247
          |:||:|||:||   | ::|  ||  ||||||||   :|:||  | | |||||||||:|||:
Db    170 TEVVRRCPHHERCSD-SDG-LAPPQHLIRVEGNLRVEYLDDRNTFRHSVVVPYEPPEVGS 227

Qy    248 EFTTILYNFMCNSSCVGGMNRRPILIIITLEMRDGQVLGRRSFEGRICACPGRDRKADED 307
          : ||| ||:||||||:||||||||| |||||   | :||| ||| |:||||||||: :|:
Db    228 DCTTIHYNYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVCACPGRDRRTEEE 287

Qy    308 HYREQQALNESSAKNG--------AASKRAFKQSPPAVPALGAGVKKRRHGDEDTYYLQV 359
          : |          | |         ::|||   :  : |       |::  | : : ||:
Db    288 NLR----------KKGEPHHELPPGSTKRALPNNTSSSPQ-----PKKKPLDGEYFTLQI 332

Qy    360 RGRENFEILMKLKESLELME 379
          |||| ||:  :| |:||| :
Db    333 RGRERFEMFRELNEALELKD 352


RESULT 14
R22238
ID   R22238 standard; Protein; 393 AA.
AC   R22238;
DT   23-JUL-1992 (first entry)
DE   Sequence of 53 kD cellular protein.
KW   Cancer therapy; cancer suppressor gene; oncogenesis.
OS   Homo sapiens.
PN   EP-475623-A.
PD   18-MAR-1992.
PF   23-AUG-1991; 307791.
PR   24-AUG-1990; US-573405.
PA   (REGC ) UNIV OF CALIFORNIA.
PI   Lee WH, Chen PL;
DR   WPI; 92-090221/12.
DR   N-PSDB; Q22995.
PT   Cloned p53 cDNA and protein prods. - for suppression of
PT   neoplastic phenotype e.g. in osteo-sarcuma(s), leukaemia(s),
PT   lymphoma(s), etc.
PS   Claim 2; Page 14; 25pp; English.
CC   p53 cDNA, or its gene prods., can be used to suppress and eradicate
CC   cancers caused by defective, mutant or absent cancer suppressor
CC   genes. Variant forms of p53 are found in human breast, lung or
CC   colon carcinoma, lymphoma, leukaemia, etc., suggesting that mutation
CC   of the p53 genes is involved in oncogenesis. Specifically 273 Arg
CC   is replaced by 273 His, a mutation found exclusively in tumour cells.
SQ   Sequence  393 AA;

  Query Match             21.4%;  Score 724.5;  DB 1;  Length 393;
  Best Local Similarity   41.0%;  Pred. No. 2.8e-55;
  Matches  157;  Conservative   57;  Mismatches  104;  Indels   65;  Gaps    9;

Qy     14 TFEHLWSSLEPDSTYFDLPQSSRGNNEVVGGTDSSMDVFHLEGMTTSVMAQFNLLSSTMD 73
          ||  ||  |  ::    ||                          : |    |    ::
Db     18 TFSDLWKLLPENNVLSPLP-------------------------SQAMDDLMLSPDDIE 51

Qy     74 QMSSRAASASPYTPEHAASVPTHSPYAQPSSTFDT-MSPAPV--------IPSNTDYPGP 124
          |  :          |: |  :|  :|   |:    |  :|||          :||   | |
Db     52 QWFTEDPG-----PDEAPRMPEAAPRVAPAPAAPTPAAPAPAPSWPLSSSVPSQKTYQGS 106

Qy    125 HHFEVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYKKA 184
          : | : |  |-|||| | |||| | |::||:|||||:|: | : ||||| :||| :||::
Db    107 YGFRLGFLHSGTAKSVTCTYSPALNKMFCQLAKTCPVQLWVDSTPPPGTRVRAMAIYKQS 166

Qy    185 EHVTDVVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPYEPPQ 244
          :|:|:||:||||:||   | ::|  ||  ||||||||   :|:||  | | |||||||||:
Db    167 QHMTEVVRRCPHHERCSD-SDG-LAPPQHLIRVEGNLRVEYLDDRNTFRHSVVVPYEPPE 224

Qy    245 VGTEFTTILYNFMCNSSCVGGMNRRPILIIITLEMRDGQVLGRRSFEGRICACPGRDRKA 304
          ||:: ||| ||:||||||:||||||||| |||||   | :||| ||| |:||||||||:
Db    225 VGSDCTTIHYNYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVCACPGRDRRT 284

Qy    305 DEDHYREQQALNESSAKNG--------AASKRAFKQSPPAVPALGAGVKKRRHGDEDTYY 356
          :|:: |          | |         ::|||   :  : |       |::  | : :
Db    285 EEENLR----------KKGEPHHELPPGSTKRALPNNTSSSPQ-----PKKKPLDGEYFT 329

Qy    357 LQVRGRENFEILMKLKESLELME 379
          ||:|||| ||:  :| |:||| :
Db    330 LQIRGRERFEMFRELNEALELKD 352


RESULT 15
R26758
ID   R26758 standard; peptide; 393 AA.
AC   R26758;
DT   09-FEB-1993 (first entry)
DE   p53.
KW   Point mutation; translocation; proto-oncogene; cancer;
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KW   antigen-presenting cell; T-cell; HLA.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   misc_difference 273
FT                   /label= mutation
FT                   /note= "Arg -> any amino acid except Arg, see CC"
PN   GB2253211-A.
PD   02-SEP-1992.
PF   26-FEB-1992; 004098.
PR   26-FEB-1991; GB-003974.
PA   (NHYD ) NORSK HYDRO AS.
PI   Eriksen JA, Gaudernack G, Geddedahl T;
DR   WPI; 92-294575/36.
PT   Synthetic oncogene-protein peptide - used for treating and
PT   vaccinating against cancers
PS   Disclosure; Page 10; 78pp; English.
CC   New peptides, which have a point mutation or translocation compared to
CC   the corresp. fragment of the proto-oncogene prod., correspond to,
CC   completely cover or are active fragments of a processed oncogene protein
CC   fragment as presented by a cancer cell or other antigen-presenting cell
CC   and are capable of inducing a specific T-cell response to the actual
CC   oncogene protein fragment as produced by the cell and processed and
CC   presented in the HLA mol.
CC   For example, a peptide fragment of p53 comprising at least
CC   mutations in position 273, in which position any amino acid except Arg
CC   may be located.  The p53 sequence below was not disclosed in the
CC   specification, but retrieved by the indexer from Swiss-prot P04637.
SQ   Sequence   393 AA;


  Query Match             21.4%;  Score 724.5;  DB 1;  Length 393;
  Best Local Similarity   42.1%;  Pred. No. 2.8e-55;
  Matches  160;  Conservative   58;  Mismatches  103;  Indels   59;  Gaps   10;

Qy      14 TFEHLWSSLEPDSTYFDLPQSSRGNNEVVGGTDSSMDVFHLEGMTTSVMAQFNLLSSTMD 73
           ||  ||  |  ::    ||  |:  ::::   |              : |:       |
Db      18 TFSDLWKLLPENNVLSPLP--SQAMDDLMLSPDD-------------IEQWFTEDPGPD 61

Qy      74 QMSSRAASASPYTPEHAASVPTHSPYAQPSSTFDTMSPAP------VIPSNTDYPGPHHF 127
           :      :| |  |  ||  |     | |       :|||       :||   | | : |
Db      62 EAPRMPEAAPPVAPAPAAPTP-----AAP-------APAPSWPLSSSVPSQKTYQGSYGF 109

Qy     128 EVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYKKAEHV 187
            : |  | |||| | |||| | |::||:|||||:|: | : ||||| :||| :||:::|:
Db     110 RLGFLHSGTAKSVTCTYSPALNKMFCQLAKTCPVQLWVDSTPPPGTRVRAMAIYKQSQHM 169

Qy     188 TDVVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPYEPPQVGT 247
           .|:||:|||:||   | ::|  ||  |||||||   :|:||  | | |||||||||:||:
Db     170 TEVVRRCPHHERCSD-SDG-LAPPQHLIRVEGNLRVEYLDDRNTFRHSVVVPYEPPEVGS 227

Qy     248 EFTTILYNFMCNSSCVGGMNRRPILIIITLEMRDGQVLGRRSFEGRICACPGRDRKADED 307
           : ||| ||:|||||:|||||||| |||||   | :||| ||| |:||||||||: :|:
Db     228 DCTTIHYNYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVCACPGRDRRTEEE 287

Qy     308 HYREQQALNESSAKNG--------AASKRAFKQSPPAVPALGAGVKKRRHGDEDTYYLQV 359
           : |          | |         ::|||   :  : |       |::  | : : ||:
Db     288 NLR----------KKGEPHHELPPGSTKRALPNNTSSSPQ-----PKKKPLDGEYFTLQI 332

Qy     360 RGRENFEILMKLKESLELME 379
           |||| ||:  :| |:||| :
Db     333 RGRERFEMFRELNEALELKD 352


Search completed: April 25, 2000, 20:10:16
Job time: 5194 sec
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